



ENTERED 1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/657,986B

DATE: 03/22/2002

TIME: 14:15:57

Input Set : A:\Sequence_listing.asc

Output Set: N:\CRF3\03222002\I657986B.raw

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APR 01 2002

TECH CENTER 1600/2900

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3 <110> APPLICANT: Madison, Edwin L.
4   Semple, Joseph Edward
5   Coombs, Gary Samuel
6   Reiner, John Eugene
7   Ong, Edgar O.
8   Araldi, Gian Luca
10 <120> TITLE OF INVENTION: Inhibitors of Serine Protease Activity of Matriptase or
11   MTSP1
13 <130> FILE REFERENCE: Corvas 255/049
15 <140> CURRENT APPLICATION NUMBER: 09/657,986B
16 <141> CURRENT FILING DATE: 2000-09-08
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 726
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo Sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: misc_feature
29 <223> OTHER INFORMATION: Nucleic acid sequence of protease domain of MTSP1
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35 ctgggccagg gccacatctg cgggtgcttcc ctcatctctc ccaactggct ggtctctgcc      120
37 gcacactgct acatcgatga cagaggattc aggtactcag accccacgca gtggacggcc      180
39 ttctctgggt tgcacgacca gagccagcgc agcgccctct ggggtgcagga gcgcaggctc      240
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43 ctggagctgg agaaaccggc agagtacagc tccatggtgc ggcccatctg cctgccggac      360
45 gcttcccatg tcttccctgc cggcaaggcc atctgggtca cgggctgggg acacaccag      420
47 tatggaggca ctggcgcgct gatcctgcaa aagggtgaga tccgcgtcat caaccagacc      480
49 acctgcgaga acctcctgcc gcagcagatc acgccgcgca tgatgtgctt gggcttcctc      540
51 agcggcgggc tggactcctg ccagggtgat tccggggggac ccctgtccag cgtggaggcg      600
53 gatgggcgga tcttccaggc cgggtgtggtg agctggggag acggctgcgc tcagaggaac      660
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57 gtatag                                           726
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61 <211> LENGTH: 241
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63 <213> ORGANISM: Homo Sapiens
65 <400> SEQUENCE: 2
67 Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
68 1           5           10           15
70 Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
71           20           25           30

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73 Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
74           35           40           45
76 Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
77           50           55           60
79 His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
80 65           70           75           80
82 Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
83           85           90           95
85 Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
86           100          105          110
88 Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
89           115          120          125
91 Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
92           130          135          140
94 Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
95 145          150          155          160
97 Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
98           165          170          175
100 Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
101           180          185          190
103 Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
104           195          200          205
106 Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
107           210          215          220
109 Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
110 225          230          235          240
112 Val

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115 <210> SEQ ID NO: 3

116 <211> LENGTH: 23

117 <212> TYPE: DNA

118 <213> ORGANISM: Artificial Sequence

120 <220> FEATURE:

121 <223> OTHER INFORMATION: Description of artificial sequence: PC-3 sscDNA sense

122 oligonucleotide primer

W--> 124 <221> NAME/KEY: misc_feature

125 <222> LOCATION: (0)...(0)

126 <223> OTHER INFORMATION: N=Inosine

W--> 128 <400> 3

W--> 130 tggtrtnvtnw sngcnrcnca ytg

23

132 <210> SEQ ID NO: 4

133 <211> LENGTH: 30

134 <212> TYPE: DNA

135 <213> ORGANISM: Artificial Sequence

137 <220> FEATURE:

138 <223> OTHER INFORMATION: Description of artificial sequence: PC-3 sscDNA anti-sense

139 oligonucleotide primer

W--> 141 <221> NAME/KEY: misc_feature

142 <222> LOCATION: (0)...(0)

143 <223> OTHER INFORMATION: N=Inosine

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154 <220> FEATURE:
155 <223> OTHER INFORMATION: Description of artificial sequence:
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168 <220> FEATURE:
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188 gaggttctcg caggtggtct ggttg 25
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192 <211> LENGTH: 39
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194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
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206 <211> LENGTH: 36
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208 <213> ORGANISM: Artificial Sequence
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214 <400> SEQUENCE: 9
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219 <210> SEQ ID NO: 10
220 <211> LENGTH: 9

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221 <212> TYPE: PRT
222 <213> ORGANISM: Homo Sapiens
224 <400> SEQUENCE: 10
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227 1 5
229 <210> SEQ ID NO: 11
230 <211> LENGTH: 726
231 <212> TYPE: DNA
232 <213> ORGANISM: Homo Sapiens
234 <220> FEATURE:
235 <221> NAME/KEY: misc_feature
236 <223> OTHER INFORMATION: Nucleic acid sequence of protease domain of MTSP1
238 <400> SEQUENCE: 11
240 caacaacccc cgtgcctacg cctactcccg ctcaccggga ccgtccattc ggacgtacga 60
242 gacccggtcc cgggtgtagac gccacgaagg gagtagagag ggttgaccga ccagagacgg 120
244 cgtgtgacga tgtagctact gtctcctaag tccatgagtc tgggggtgcgt cacctgccgg 180
246 aaggacccga acgtgctggt ctcggtcgcg tcgcggggac cccacgtcct cgcgtccgag 240
248 ttgcgtagt agaggggtggg gaagaagtta ctgaagtgga agctgatact gtagcgcgac 300
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254 atacctccgt gaccgcgcga ctaggacgtt ttcccactct aggcgcagta gttggtctgg 480
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258 tcgccgcgc acctgaggac ggtcccacta aggccccctg gggacaggtc gcacctccgc 600
260 ctacccgcct agaaggtccg gccacaccac tcgaccctc tgccgacgcg agtctccttg 660
262 ttcggtccgc acatgtgttc cgaggggagac aaagccctga cctagtttct cttgtgaccc 720
264 catatc 726

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VERIFICATION SUMMARY

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Input Set : A:\Sequence_listing.asc

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L:124 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:128 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:141 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:145 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0